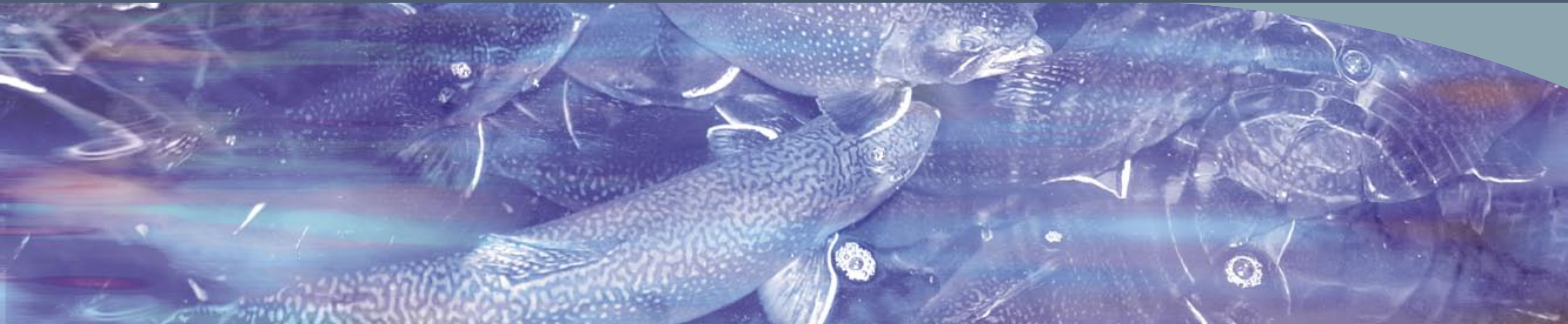


Situated at the eastern end of the Blue Ridge Mountains and within 60 miles (96.6 km) of Washington, D.C., two high gradient streams and their tributaries support 17 known species of fish in Catoctin Mountain Park. The fantail darter (*Etheostoma flabellare*), mottled sculpin (*Cottus bairdii*), cutlips minnow (*Exoglossum maxillingua*), and dace (*Rhinichthys* and *Clinostomus* spp.) are commonly found, while elusive species like the American eel (*Anguilla rostrata*) often escape even the most careful observer. However, it is the Park's populations of trout that attract the most attention.

Big Hunting Creek in the Park has played a prominent role in the development of recreational trout fishing in Maryland. The stream has long been popular among fly fishermen, who are attracted by brook (*Salvelinus fontinalis*), brown (*Salmo trutta*), and rainbow trout (*Oncorhynchus mykiss*). Big Hunting Creek was the first in the State of Maryland to be designated as a "Fly-Fishing-Only" stream. Later, it became Maryland's first "Catch-and-Release" trout stream. Outside the Park and below the dam that forms Hunting Creek Lake, the Maryland Department of Natural Resources stocks limited numbers of hatchery-raised rainbow and brook trout to enhance the stream's recreational fishing. The lake is managed by Cunningham Falls State Park, which is adjacent to Catoctin Mountain Park.

The population of brook trout is very special because it is the only trout species native to this region. Both brook and brown trout spawn in the headwaters of Big Hunting and Owens Creeks, but only brook trout spawn in the headwaters of Still Creek, which is a tributary to Big Hunting Creek. The Park does not stock brook trout into its creeks; its fish are wild and naturally occurring. Brook trout inhabit pristine stream environments, and its presence or absence is often perceived as an indicator of ecosystem integrity. Owens Creek is located on the northern side of the Park and contains populations of brown and brook trout, but the brook trout are more abundant.

## NATIVE BROOK TROUT THEY'RE NOT ALL THE SAME







**Top:** Staff at Leetown Science Center, U.S. Geological Survey, prepares samples for genetic analysis; **Bottom:** Small amounts of tissue collected from brook trout fins are used for analysis of variation in microsatellite DNA; **Opposite page:** Large samples allow for comparison of genetic variation within and between populations.

Natural resource managers in the National Park Service respond to many different management needs, including meeting the recreation needs of the American people while maintaining and enhancing the integrity of our ecosystems. Our goal is to provide for sustainable use of natural resources for recreation while preserving the resources.

Maintaining the genetic integrity of native, wild populations is very important in the conservation biology of a species. The genetic variation that exists in a population is the product of thousands of years of evolution and is critical to a population's ability to adapt to changes to its environment. Heritable genetic information offers an objective means of depicting management units and provides an evolutionary framework from which to develop and evaluate conservation priorities. Conserving biological diversity helps preserve species and prevents the disruption of natural processes such as species interactions and evolution.

The number of wild brook trout populations in the United States has been dramatically reduced as a result of overexploitation, competition from non-native fish, and habitat loss from such human-caused factors as deforestation, hydroelectric

power development, and acid rain. The Air Resources Program at the Center for Urban Ecology works with the Park to monitor pollutants such as mercury and sulfur dioxide threats to the aquatic wildlife within the Park's streams. As a result of declining numbers of fish, the management and restoration of wild brook trout populations are important goals throughout their native range.

“ Maintaining the genetic integrity of native, wild populations is very important in the conservation biology of a species. ”

While anecdotal accounts from the 1930's indicate that brook trout were once abundant in the Park, some fisheries reports indicate the absence of brook trout from Owens Creek in the 1970's. It is difficult to pinpoint what happened to the brook trout at that time; there is no historical documentation of restocking. Finding clues to the origins of current brook trout populations requires the Park to identify the genetic variation in the brook trout and to understand the DNA variation of brook trout populations outside of the Park. Relatively large genetic differences can occur over short geographic distances because brook trout are territorial and live in local breeding groups in various watersheds, streams, and pools (Perkins et al. 1993).

## Genetics Studies of Brook Trout in National Parks

The native range of brook trout (*Salvelinus fontinalis*) originally extended throughout eastern Canada and the northeastern and central United States. Brook trout is native to 18 National Parks in the United States, including Catoctin Mountain Park. With the exception of Great Smoky Mountains National Park, little was known about the ecological and evolutionary relationships among brook trout found in streams within or outside of park boundaries. Traditionally, National Parks based brook trout management practices on geographic location and did not take genetic relatedness among populations into account. To address

this research need, the National Park Service collaborated with the U.S. Geological Survey, Biological Resources Discipline to survey the genetic variation in over 5,000 brook trout. These wild brook trout were collected from the major drainages within five National Parks: Acadia National Park, Catoctin Mountain Park, Shenandoah National Park, Great Smoky Mountains National Park, and Isle Royale National Park, and from several other populations located outside park boundaries. This survey identified a high degree of genetic diversity and differentiation at three different levels studied: populations, Parks, and drainages (King 2005).

Increased interest in restoring and enhancing brook trout requires a better understanding of the partitioning of genetic variation among different Park drainages and the effects of any past restoration effort.

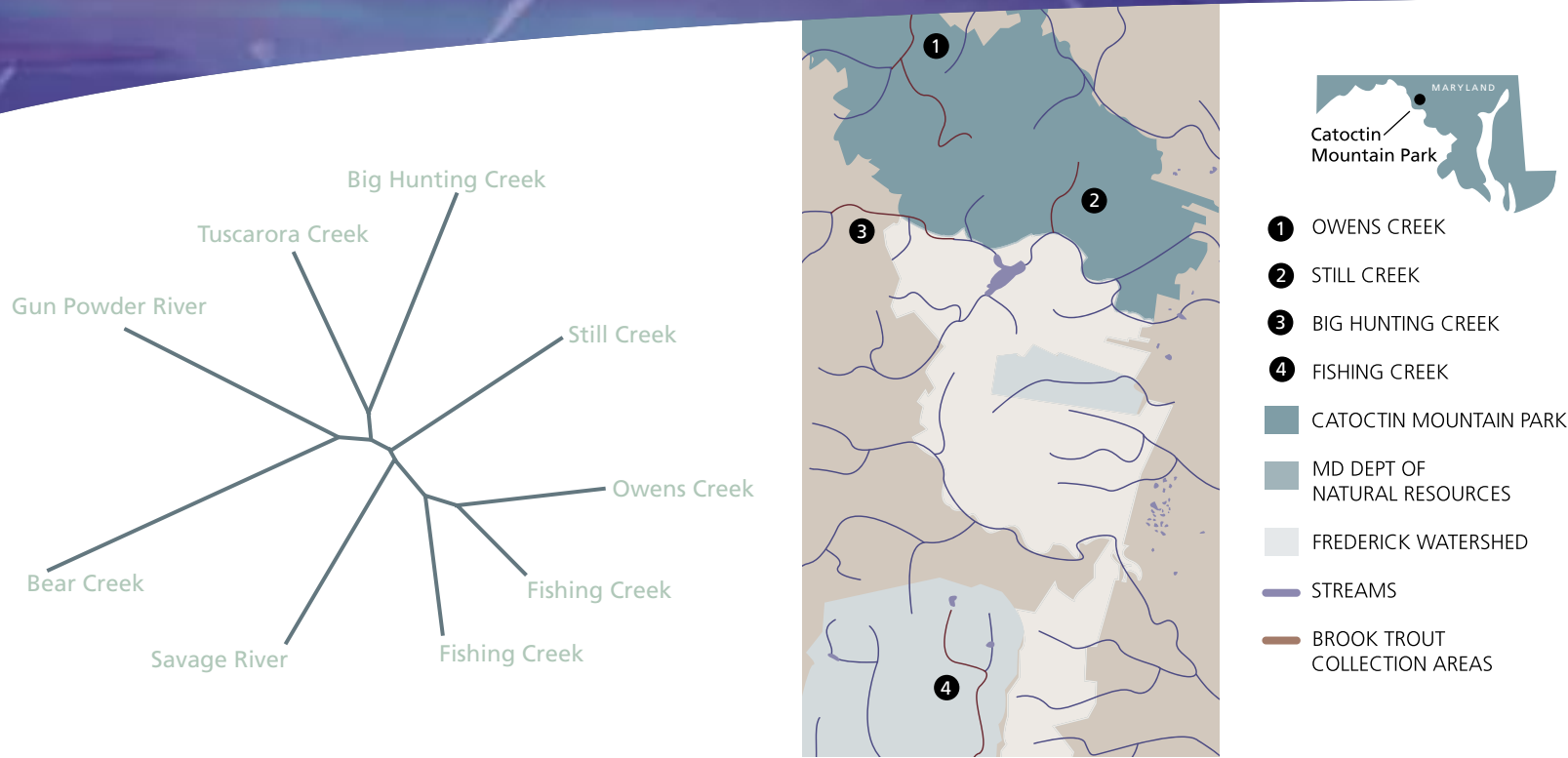
The traditional method of addressing the decline of native populations has been hatchery supplementation. However, mixing genetically divergent stocks of brook trout has serious potential problems, including the loss of local adaptation, disruption of locally-adapted gene combinations, and the spread of pathogens. Declines in the number of breeding individuals in populations can

result in reduced levels of genetic diversity among wild brook trout populations. It is estimated that less than 5% of brook trout populations in the many inland streams of the northeastern United States may still contain wild fish (Quattro et al. 1990, McCracken et al. 1993, Perkins et al. 1993). With this in mind, three important questions arise: is the population of brook trout in the Park still wild, and what are the genetic relationships among populations within the Park and those populations adjacent to the Park?

Obtaining genetic information is crucial for brook trout management. Future needs may call for using existing populations to expand the range of brook trout in Park streams or reintroducing brook trout following an environmental disaster. Brook trout were missing from Owens Creek in the Park in the 1970's; this loss could happen again. Wild brook trout remained in upper Big Hunting Creek and in its tributary, Still Creek. It is important to know the genetics of existing populations before any of these actions occur. For instance, if the genetic diversity is significantly different among populations, then maintaining separate populations may be better than mixing them.







### The Unrooted Tree

This unrooted, Neighbor-Joining tree (or phenogram) shows the genetic distances between brook trout (*Salvelinus fontinalis*) from nine locations in Maryland, encompassing the drainage systems in and around Catoctin Mountain Park. It was possible to identify each population examined; that is, there is not one homogeneous gene pool for all brook trout inhabiting Catoctin Mountain Park or the other drainages in Maryland. The most genetically different populations are those along the Atlantic slope drainage (Bear Creek of the Youghiogheny River) and those within the interior basin drainage (Big Hunting Creek, Still Creek, and Owens Creek at Catoctin Mountain Park) (King and Julian (2000). King and Julian identified the collections from Fishing Creek and Owens Creek as the most genetically similar populations. In fact, they observed distinctly different branches on the tree for all collections except for those two streams.

To determine genetic diversity across the range of brook trout, Dr. Tim King with the U.S. Geological Survey, Biological Resources Discipline, Leetown Science Center conducted a survey within the Park and compared these Park populations and others. The Park and Maryland Department of Natural Resources staffs collected small amounts of tissue (fin clips) nondestructively from brook trout in three Park

streams: Owens Creek, Big Hunting Creek upstream of Route 77, and Still Creek. Outside of the park, they also collected tissue samples from Fishing Creek, which is located just south of Cunningham Falls State Park. In addition, Dr. Ray Morgan from the Appalachian Laboratory, University of Maryland, Frostburg, Maryland, collected tissue samples from five populations in Maryland streams. These included Bear

Creek (Youghiogheny River), Savage River (Potomac River), Gunpowder River, the left fork of Fishing Creek (Monocacy River), and Tuscarora Creek (Monocacy River).

Genetic diversity was measured as variation in microsatellite DNA. These are short pieces of DNA that occur as variable numbers of repeated DNA sequences. Molecular genetics has recently achieved an

important place in contemporary conservation biology as a robust tool for identifying fine-scale population structure and determining the degree of reproductive isolation among populations. The molecular survey was completed in 2004. This study represented the first survey of microsatellite DNA variation in Maryland brook trout.

Dr. King’s genetic analysis revealed a high degree of population subdivision and large genetic distances among all watersheds studied. Scientists at Dr. King’s lab screened 325 brook trout from the nine locations for eight microsatellite DNA loci. Furthermore, the resulting data set contained sufficient allelic diversity to reveal unique multilocus genotypes for all individuals sampled. The pattern of genetic variation observed suggests a series of phylogeographic breaks that correspond to the major drainages surveyed, which may indicate local (or regional) adaptive significance and may reveal diverging evolutionary pathways.

The genetic analysis showed that Owens Creek within the Park was genetically closest to Fishing Creek located outside of the Park. The genetic data from this study support the reports of reintroductions of wild brook trout into Owens Creek from Fishing Creek sometime in the recent past. And, since considerable genetic differentiation exists between Still Creek and Big Hunting Creek, it may be that Cunningham Falls and the park reservoir dam serve as physical barriers to gene flow.

From this study, we learned that Catoctin Mountain Park is still home to a remarkable population of wild, native brook trout. This is key information for park managers to use when reviewing plans for restoration, road and trail construction, responding to hazardous materials spills, and for routine Park maintenance practices. This information will better direct the long term monitoring of the fish populations of the Park.

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### CENTER FOR URBAN ECOLOGY

**Air Resources Program** Air pollutants do not just make the air murky and unhealthy to breathe. They also can harm ecosystems by acidifying and enriching both soils and water bodies (via nitrogen and sulfur deposition), by damaging and retarding growth in plants (via ozone deposition), and even by poisoning fish and the organisms that feed on them (via mercury deposition). Thus, air pollutants are a threat to brook trout populations. To protect park resources and predict effects of air pollutants on natural resources in the National Capital Region, the Air Resources Program at the Center for Urban Ecology coordinates with national-scale air quality monitoring programs both within and outside the National Park Service. These include:

- Interagency Monitoring of Protected Visual Environments (IMPROVE)
- Clean Air Status and Trends Network (CASTNET)
- National Atmospheric Deposition Program (NADP).